

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 16:07:30 ; Search time 20 Seconds
(without alignment)
1254.554 Million cell updates/sec

Title: US-09-988-971-2

Perfect score: 261
Sequence: 1 MSLPSRRKSLPSPSSSV.....RESLSFYISLNDEAVSIDDA 261

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	3.4	505	2 I37206	protein-tyrosine k
2	8	3.1	151	2 S10084	hypothetical 16K p
3	8	3.1	217	2 S26050	growth factor rece
4	8	3.1	217	2 A54688	modular adaptor Gr
5	8	3.1	217	2 A43321	growth factor rece
6	8	3.1	217	2 JT0664	growth factor rece
7	8	3.1	281	2 A57152	src-like adaptor p
8	8	3.1	461	2 A57463	p55PIK - mouse
9	8	3.1	503	1 UQ1321	protein-tyrosine k
10	8	3.1	503	1 TVMSHC	protein-tyrosine k
11	8	3.1	505	1 TVHUC	protein-tyrosine k
12	8	3.1	507	1 A39939	protein-tyrosine k
13	8	3.1	512	1 TVHULY	protein-tyrosine k
14	8	3.1	512	1 I56160	protein-tyrosine k
15	8	3.1	512	1 A39719	protein-tyrosine k
16	8	3.1	512	2 I45552	protein-tyrosine k
17	8	3.1	517	2 A43807	protein-tyrosine k
18	8	3.1	517	2 S24547	protein-tyrosine k
19	8	3.1	529	1 TVHUF	protein-tyrosine k
20	8	3.1	534	1 A44991	protein-tyrosine k
21	8	3.1	575	2 T30021	protein-tyrosine k
22	8	3.1	743	2 T38674	hypothetical prote
23	8	3.1	93	2 D48059	probable membrane
24	7	2.7	106	2 S77055	oncoprotein zn-fyc
25	7	2.7	114	2 T44547	hypothetical prote
26	7	2.7	115	2 AB1172	hypothetical prote
27	7	2.7	117	2 T17315	hypothetical prote
28	7	2.7	118	2 AC1449	hypothetical prote
29	7	2.7	120	2 A48837	hypothetical prote
					subgroup A Rous sa

30	7	2.7	116	2 H8763	hypothetical prote
31	7	2.7	117	2 S37353	nodulin (clone GME
32	7	2.7	137	2 PC4110	transcription regu
33	7	2.7	140	2 E97462	organic hydroperox
34	7	2.7	140	2 AC3680	organic hydroperox
35	7	2.7	157	2 B48837	subgroup A Rous sa
36	7	2.7	166	2 T49489	related to H+tran
37	7	2.7	180	2 C83573	hypothetical prote
38	7	2.7	188	2 F95944	hypothetical prote
39	7	2.7	199	2 T46076	hypothetical prote
40	7	2.7	193	2 C75194	hypothetical prote
41	7	2.7	198	2 T37263	hypothetical prote
42	7	2.7	200	2 F71495	probable tyrosine
43	7	2.7	202	2 H81653	probable n-acetyl
44	7	2.7	210	2 B60030	conserved hypotet
45	7	2.7	217	2 B88316	gene B protein - a
46	7	2.7	217	2 B90968	unknown protein en
47	7	2.7	219	2 A86649	hypothetical prote
48	7	2.7	236	2 A12759	hypothetical prote
49	7	2.7	245	2 G75422	arsenical resisten
50	7	2.7	248	2 G97540	hypothetical prote
51	7	2.7	252	2 S25950	arsh-like protein
52	7	2.7	259	2 B37410	cytochrome-c oxida
53	7	2.7	269	2 A95906	mastocytoma protei
54	7	2.7	275	2 H89880	hypothetical prote
55	7	2.7	278	2 E70244	hypothetical prote
56	7	2.7	278	2 C70244	antigen, p35 homol
57	7	2.7	278	2 E75546	conserved hypotet
58	7	2.7	284	2 T39813	hypothetical prote
59	7	2.7	287	2 F81705	conserved hypotet
60	7	2.7	294	2 D83393	methyl-accepting c
61	7	2.7	294	2 G81318	hypothetical prote
62	7	2.7	327	2 H72530	hypothetical prote
63	7	2.7	312	2 C84511	hypothetical prote
64	7	2.7	315	2 AE0166	probable virulence
65	7	2.7	318	2 H86342	hypothetical prote
66	7	2.7	335	2 D75279	hypothetical prote
67	7	2.7	334	2 T36485	conserved hypotet
68	7	2.7	346	2 T45069	probable arac-fam1
69	7	2.7	370	2 H70423	8-hydroxy-guanine
70	7	2.7	387	2 A83388	oxygen-independent
71	7	2.7	387	2 AE2950	probable MPS trans
72	7	2.7	404	2 AE2950	RND multidrug effl
73	7	2.7	405	2 F59100	hypothetical prote
74	7	2.7	419	2 T49459	hypothetical prote
75	7	2.7	419	2 T51715	sigma-like factor
76	7	2.7	423	2 F08332	hypothetical prote
77	7	2.7	427	2 F08332	hypothetical prote
78	7	2.7	434	2 G97049	hypothetical prote
79	7	2.7	453	2 C83008	xre family DNA-bin
80	7	2.7	458	2 D82974	conserved hypotet
81	7	2.7	467	2 D95253	L-serine dehydrata
82	7	2.7	479	2 H97773	L-fucose kinase
83	7	2.7	482	2 B98118	osmolarity sensor
84	7	2.7	482	2 A83655	thiaminokinase (EC
85	7	2.7	484	2 C75609	lysine decarboxyla
86	7	2.7	506	2 B55210	amino acid ABC tra
87	7	2.7	518	2 A82475	hem protein - Ana
88	7	2.7	521	2 G75532	polynucleotide synt
89	7	2.7	528	2 T01242	hypothetical prote
90	7	2.7	543	2 A53310	peptide transport
91	7	2.7	544	2 I51593	hypothetical prote
92	7	2.7	552	2 A56560	phoromone CADI bin
93	7	2.7	610	2 S59394	protein-tyrosine k
94	7	2.7	620	2 T15273	zinc finger protei
95	7	2.7	631	2 C64074	protein kinase RCK
96	7	2.7	653	2 C64074	hypothetical prote
97	7	2.7	653	1 DN2PPA	hypothetical prote
98	7	2.7	658	2 T46359	polyadenylate-bind
99	7	2.7	673	2 T34317	hypothetical prote
100	7	2.7	702	2 T05619	protein-tyrosine-p
					hypothetical prote
					arginine decarboxy

ALIGNMENTS

RESULT 1

137206

Protein-tyrosine kinase (EC 2.7.1.112) blk - human

C/Species: Homo sapiens (man)

C/Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 04-Mar-2000

C/Accession: I37206; S51647

R/Islam, K.B.; Rabbani, H.; Larsson, C.; Sanders, R.; Smith, C.I.

J. Immunol. 154, 1265-1272, 1995

A/Title: Molecular cloning, characterization, and chromosomal localization of a human tyrosine kinase gene

A/Reference number: I37206; MUID:95123078; PMID:782795

A/Accession: I37206

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-505 <RES>

A/Cross-references: EMBL:233998; NID:9601951; PIDN:CAA83965.1; PID:9601952

C/Genetics:

A/Status: GDB:BLK

A/Map position: 8p23-8p22

C/Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology

C/Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphotransferase; tyrosine

F/65-113/Domain: SH3 homology <SH3>

F/124-220/Domain: SH2 homology <SH2>

F/239-497/Domain: protein kinase homology <KIN>

F/247-255/Region: protein kinase ATP-binding motif

F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F/269/Active site: Lys #status predicted

Query Match

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 165 TFPSSALV 173

Db 194 TFPSSALV 202

RESULT 2

S10084

Hypothetical 16k protein - wheat insertion sequence WIS1

C/Species: Triticum aestivum (common wheat)

C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 29-Oct-1999

C/Accession: S10084

R/Martensen, R.A.; Baulcombe, D.C.

Mol. Gen. Genet. 217, 401-410, 1989

A/Title: An unusual wheat insertion sequence (WIS1) lies upstream of an alpha-amylase gene

A/Reference number: S10084; MUID:89364725; PMID:2549380

A/Accession: S10084

A/Status: preliminary; translation not shown

A/Molecule type: DNA

A/Cross-references: EMBL:X15870; NID:921903; PIDN:CAA33880.1; PID:921904

C/Genetics:

A/Mobile element: insertion sequence WIS1

C/Superfamily: wheat insertion sequence WIS1 hypothetical 16k protein

Query Match

Best Local Similarity 100.0%; Pred. No. 4.4;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 LBPSSLS 18

Db 22 LBPSSLS 29

RESULT 3.

S26050

Growth factor receptor-bound protein, GRB2 - rat

N/Alternate names: Ash-m; Ash-s; gene ash protein

C/Species: Rattus norvegicus (Norway rat)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C/Accession: S26050; I55429; I70120

R/Matucka, K.; Shibata, M.; Yamakawa, A.; Takenawa, T.

Proc. Natl. Acad. Sci. U.S.A. 89, 9015-9019, 1992

A/Title: Cloning of ASH, a ubiquitous protein composed of one src homology region (SH) 2

A/Reference number: S26050; MUID:93028395; PMID:1384039

A/Accession: S26050

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-217 <MAT>

A/Cross-references: EMBL:X62853; NID:955762; PIDN:CAA44665.1; PID:955763

R/Matucka, K.; Fukuchi, T.; Hosoya, H.; Shirasawa, T.; Matucka, K.; Miki, H.; Takenawa, T.

J. Biol. Chem. 270, 13733-13739, 1995

A/Title: Splicing isoforms of rat Ash/Grb2. Isolation and characterization of the cDNA

A/Reference number: I55429; MUID:95293967; PMID:7775428

A/Accession: I55429

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-156, 171-217 <RES>

A/Cross-references: GB:ID9847; NID:914956; PIDN:BA008645.1; PID:914957

A/Accession: I70120

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-59 <RES2>

A/Cross-references: GB:ID9847; NID:914956; PIDN:BA008646.1; PID:914961

C/Superfamily: crk transforming protein; SH2 homology; SH3 homology

C/Keywords: growth factor receptor

F/5-53/Domain: SH3 homology <SH31>

F/60-150/Domain: SH2 homology <SH2>

F/163-210/Domain: SH3 homology <SH32>

Query Match

Best Local Similarity 100.0%; Pred. No. 6.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 116 GAFLIRS 123

Db 81 GAFLIRS 88

RESULT 4

A54688

Modular adaptor Grb2 - mouse

C/Species: Mus musculus (house mouse)

C/Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 21-Jan-2000

C/Accession: A54688

R/Suen, K.L.; Bustelo, X.R.; Pawson, T.; Barbacid, M.

Mol. Cell. Biol. 13, 5500-5512, 1993

A/Title: Molecular cloning of the mouse grb2 gene: differential interaction of the Grb2

A/Reference number: A54688; MUID:93360985; PMID:7689150

A/Accession: A54688

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-217 <SUE>

A/Cross-references: GB:U07617; NID:9464004; PIDN:AA040022.1; PID:9464005

C/Genetics:

A/Status: grb2

C/Superfamily: crk transforming protein; SH2 homology; SH3 homology

F/5-53/Domain: SH3 homology <SH31>

F/60-150/Domain: SH2 homology <SH2>

F/163-210/Domain: SH3 homology <SH32>

Query Match

Best Local Similarity 100.0%; Pred. No. 6.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 116 GAFLIRS 123

Db 81 GAFLIRS 88

RESULT 5

A43521

growth factor receptor-bound protein 2 - human
 N:Alternate names: abundant-erc-homology (ash) protein
 N:Contains: growth factor receptor-bound protein 3-3
 C:Species: Homo sapiens (man)
 C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: A43321; A54064; A46278
 R:Lowenstein, E.J.; Daly, R.J.; Batzer, A.G.; Li, W.; Margolis, B.; Lammers, R.; Ullrich
 Cell 70: 431-442, 1992
 A>Title: The SH2 and SH3 domain-containing protein GRB2 links receptor tyrosine kinases
 A:Reference number: A43321; MUID:92354060; PMID:1322798
 A:Accession: A43321
 A:Molecule type: mRNA
 A:Residues: 1-217 <LOW>
 A:CROSS-references: GB:M96995; NID:g181975; PIDN:AAA58448.1; PID:g181976
 A:Experimental source: Brain
 A>Note: sequence extracted from NCBI backbone (NCBI:110294, NCBI:110295)
 R:Path, I.; Schweighoffer, F.; Rey, I.; Mutton, M.C.; Botziau, J.; Duchesne, M.; Tocque,
 Science 264, 971-974, 1994
 A>Title: Cloning of a Grb2 isoform with apoptotic properties.
 A:Reference number: A54064; MUID:94233382; PMID:8178156
 A:Accession: A54064
 A:Molecule type: mRNA
 A:Residues: 1-59, 101-217 <FAT>
 A:CROSS-references: GB:I29511; NID:g460667; PIDN:AA37549.1; PID:g498178
 R:Matuoka, K.; Shibata, M.; Yamakawa, A.; Takenawa, T.
 Proc Natl Acad Sci U S A 89, 9015-9019, 1992
 A>Title: Cloning of ASH, a ubiquitous protein composed of one Src homology region (SH) 2
 A:Reference number: S26050; MUID:93028395; PMID:1384039
 A:Accession: A46278
 A:Molecule type: mRNA
 A:Residues: 58-217 <MAT>
 A:CROSS-references: EMBL:X62852; NID:g28875; PIDN:CAA4664.1; PID:g28876
 C:Genetics:
 A:Gene: GDB:GRB2
 A:CROSS-references: GDB:134732; OMIM:600180
 A:Map position: 17q24-17q25
 C:Superfamily: crk transforming protein; SH2 homology; SH3 homology
 C:Keywords: alternative splicing; growth factor receptor
 F:1-217/Product: growth factor receptor-bound protein 2 #status predicted <LSF>
 F:1-59,101-217/Product: growth factor receptor-bound protein 3 #status predicted <SSF>
 F:53-53/Domain: SH3 homology <SH31>
 F:60-150/Domain: SH2 homology <SH2>
 F:163-210/Domain: SH3 homology <SH32>
 F:163-210/Domain: SH3 homology <SH32>

Query Match 3.1%; Score 8; DB 2; Length 217;
 Best Local Similarity 100.0%; Pred. No. 6.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFLIRES 123
 DB 81 GAFLIRES 88

RESULT 6
 growth factor receptor-binding protein GRB2 homolog - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 21-Jan-2000
 C:Accession: J70664
 R:Maenitius, V.M.; Merilaenen, J.; Lehto, V.P.
 Gene 134, 299-300, 1993
 A>Title: Sequence of a chicken cDNA encoding a GRB2 protein.
 A:Reference number: J70664; MUID:94085795; PMID:8262390
 A:Accession: J70664
 A:Molecule type: mRNA
 A:Residues: 1-217 <WAS>
 A:CROSS-references: GB:119258; NID:g304385; PIDN:AAA16318.1; PID:g304386
 C:Comment: GRB2 protein plays a role in mediating the critical linkage between growth fa
 C:Superfamily: crk transforming protein; SH2 homology; SH3 homology
 C:Keywords: growth factor receptor
 F:5-53/Domain: SH3 homology <SH31>
 F:60-150/Domain: SH2 homology <SH2>
 F:163-210/Domain: SH3 homology <SH32>

Query Match 3.1%; Score 8; DB 2; Length 217;
 Best Local Similarity 100.0%; Pred. No. 6.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFLIRES 123
 DB 81 GAFLIRES 88

RESULT 7
 src-like adaptor protein - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 12-Feb-1999
 C:Accession: A57152
 R:Pandey, A.; Duan, H.; Dixit, V.M.
 J. Biol. Chem. 270, 19201-19204, 1995
 A>Title: Characterization of a novel Src-like adapter protein that associates with the F
 A:Reference number: A57152; MUID:95370243; PMID:7543898
 A:Accession: A57152
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-281 <PAN>
 A:CROSS-references: GB:U29056
 C:Superfamily: SH3 homology; SH2 homology
 F:29-77/Domain: SH3 homology <SH3>
 F:84-175/Domain: SH2 homology <SH2>

Query Match 3.1%; Score 8; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 YISPRUTF 166
 DB 143 YISPRUTF 150

RESULT 8
 p53PTK - mouse
 C:Species: Mus sp. (mouse)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: A57463
 R:Pons, S.; Asano, T.; Gjaahen, E.; Miralpeix, M.; Zhang, Y.; Fisher, T.L.; Myers, M.G.
 Mol. Cell Biol 15, 4453-4465, 1995
 A>Title: The structure and function of p53PTK reveal a new regulatory subunit for phosph
 A:Reference number: A57463; MUID:95349612; PMID:7542745
 A:Accession: A57463
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-461 <RES>
 A:CROSS-references: GB:S79169; NID:g1050992; PIDN:AMB34938.1; PID:g1050993
 F:65-160/Domain: SH2 homology
 F:356-452/Domain: SH2 homology <SH2>

Query Match 3.1%; Score 8; DB 2; Length 461;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFLIRES 123
 DB 378 GAFLIRES 385

RESULT 9
 JQ1321
 protein-tyrosine kinase (EC 2.7.1.112) hck - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
 C:Accession: JQ1321; S18974
 R:Okano, Y.; Sugimoto, Y.; Fukuoka, M.; Matsui, A.; Nagata, K.; Nozawa, Y.

Qy 128 GSYSLSVR 135
 |||||
 Db 157 GSYSLSVR 164

RESULT 12

A39939

protein-tyrosine kinase (EC 2.7.1.112) [kl (similarity) - chicken
 N/Alternate names: kinase-related transforming protein (tkl); T-cell surface antigen ass
 C/Species: Gallus gallus (chicken)
 C/Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 16-Jun-2000

C/Accession: A42126; A39939
 R/Chow, L.M.; Ratcliffe, M.J.; Veillette, A.

Mol. Cell. Biol. 12, 1226-1233, 1992

A/Title: tkl is the avian homolog of the mammalian lck tyrosine protein kinase gene.
 A/Reference number: A42126; MUID:92186854; PMID:1545804

A/Accession: A42126

A/Molecule type: mRNA

A/Residues: 1-88 <CHO>

A/Cross-references: GB:M85043
 A/Note: sequence extracted from NCBI backbone (NCBI:88831, NCBI:88833)

R/Strebhardt, K.; Mullins, J.I.; Bruck, C.; Ruebsamen-Waigmann, H.
 Proc. Natl. Acad. Sci. U.S.A. 84, 8778-8782, 1987

A/Title: Additional member of the protein-tyrosine kinase family: the src-and lck-relate
 A/Reference number: A39939; MUID:88097370; PMID:3321053

A/Accession: A39939

A/Molecule type: mRNA

A/Residues: 52-507 <STR>

A/Cross-references: GB:J03579; NID:G212712; PIDN:AAA9081.1; PID:G212713

C/Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
 C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pnc
 F/125-222/Domain: SH2 homology <SH2>

F/241-499/Domain: protein kinase homology <KIN>

F/249-257/Region: protein kinase ATP-binding motif

F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F/392,503/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 3.1%; Score 8; DB 1; Length 507;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 128 GSYSLSVR 135
 |||||
 Db 159 GSYSLSVR 166

RESULT 13

TNUHUY

protein-tyrosine kinase (EC 2.7.1.112) lym, splice form A - human
 N/Contains: protein-tyrosine kinase lym, splice form B

C/Species: Homo sapiens (man)
 C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 18-Feb-2000

C/Accession: A26719; D38268; P09499; I53715
 R/Yamanashi, Y.; Fukuhide, S.I.; Semba, K.; Sukegawa, J.; Miyajima, N.; Matsubara, K.;

Mol. Cell. Biol. 7, 237-243, 1987
 A/Title: The yes-related cellular gene lym encodes a possible tyrosine kinase similar to
 A/Reference number: A26719; MUID:87172710; PMID:3561390

A/Accession: A26719

A/Molecule type: mRNA

A/Residues: 1-512 <YAM>

A/Cross-references: GB:M16038; NID:G187268; PIDN:AAA59540.1; PID:G307144

R/Pattanan, U.; Maekelae, T.P.; Allalo, R.; Lehtvaeslaine, H.; Allalo, K.
 Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990

A/Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
 A/Reference number: A38268; MUID:91062389; PMID:2247464

A/Accession: D38268
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 369-424 <PAR>

R/Bielke, W.; Ziemiecki, A.; Kappos, L.; Miescher, G.C.

Biochem. Biophys. Res. Commun. 186, 1403-1409, 1992
 A/Title: Expression of the B cell-associated tyrosine kinase gene lym in primary neurobl
 A/Reference number: P09499; MUID:92378604; PMID:1510669

A/Accession: P09499

A/Molecule type: mRNA

A/Residues: 369-424 <RIF>

A/Experimental source: neuroblastoma SK-IN cell

R/Sider, L.G.; Raben, N.; Miller, L.; Jelsema, C.
 Gene 138, 219-222, 1994

A/Title: The CDNA encoding two forms of the lym protein tyrosine kinase are expressed;
 A/Reference number: I53715; MUID:94171041; PMID:8125304

A/Accession: I53715

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-24,46-512 <RID>

A/Cross-references: GB:M79321; NID:G187270; PIDN:AA50019.1; PID:G187271

A/Experimental source: splice form B

C/Genetics:

A/Gene: GDB:LYN

A/Cross-references: GDB:120159; OMIM:165120

A/Map position: 8q13-qter

C/Function:
 A/Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP

C/Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
 C/Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote
 tyrosine-specific protein kinase

F/2-512/Product: protein-tyrosine kinase lym, splice form A #status predicted <MATA>
 F/2-24,46-512/Product: protein-tyrosine kinase lym, splice form B #status predicted <MATA>

F/70-118/Domain: SH3 homology <SH3>

F/125-226/Domain: SH2 homology <SH2>

F/245-504/Domain: protein kinase homology <KIN>

F/253-261/Region: protein kinase ATP-binding motif

F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F/3/Binding site: palmitate (Cys) (covalent) #status predicted

F/275/Active site: lys #status predicted
 F/397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 3.1%; Score 8; DB 1; Length 512;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 GAFPIRES 123
 |||||
 Db 151 GAFPIRES 158

protein-tyrosine kinase (EC 2.7.1.112) lym, splice form A - rat
 N/Contains: protein-tyrosine kinase lym, splice form B

C/Species: Rattus norvegicus (Norway rat)
 C/Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000

C/Accession: I56160; I67811; I67812
 R/Minouchi, K.; Nishikata, H.; Siriganian, R.P.

J. Immunol. 150, 222, 1993
 A/Title: Bacterially expressed rat p56lyn binds several proteins in rat basophilic leuke

A/Reference number: I56160
 A/Accession: I56160

A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA

A/Residues: 1-512 <MIN>

A/Cross-references: GB:U14951; NID:G294582; PIDN:AAA1549.1; PID:G294583
 R/Rider, L.G.; Raben, N.; Miller, L.; Jelsema, C.
 Gene 138, 219-222, 1994

A/Title: The CDNA encoding two forms of the lym protein tyrosine kinase are expressed;
 A/Reference number: I53715; MUID:94171041; PMID:8125304

A/Accession: I67811

A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA

A/Residues: 1-230,'L',232-307,'A',309-418,'Y',420-512 <RDI>
 A/Cross-references: GB:U14782; NID:G294578; PIDN:AAA20944.1; PID:G294579

A/Note: in Genbank entry RATTLYNATYR, release 116.0, PIDN:AAA20944.1, the source is desig
 A/Accession: I67812

A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-24,46-230,'I',232-307,'A',309-418,'Y',420-512 <RID2>
 A:Cross-references: GB:U14823; NID:9294580; PIDD:AAA20945.1; PID:9294581
 A>Note: in Genbank entry RNTLYNTRY, release 116.0, PIDD:AAA20945.1, the source is designated as *Rattus norvegicus* (house mouse).
 C:Superfamily: protein-tyrosine kinase src, protein kinase homology, SH2 homology, SH3 homology
 C:Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprotease
 F:2-512/Product: protein-tyrosine kinase lym, splice form A #status predicted <WAT>
 F:2-24,46-512/Product: protein-tyrosine kinase lym, splice form B #status predicted <WAT>
 F:70-118/Domain: SH3 homology <SH3>
 F:129-226/Domain: SH2 homology <SH2>
 F:245-504/Domain: protein kinase homology <KIN>
 F:253-261/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:2/5/Active site: lys #status predicted
 F:397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 3.1%; Score 8; DB 1; Length 512;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 116 GAFILRES 123
 Db 151 GAFILRES 158

RESULT 15

A39719
 A:Molecule type: mRNA
 A:Residues: 1-512 <STR1>
 A:Cross-references: GB:M64608; NID:9198938; PIDD:AAA39470.1; PID:9198939
 A:Molecule type: mRNA
 A:Residues: 1-24,46-512 <STR2>
 A:Cross-references: GB:M64608
 R:Yi, T.; Bolen, J.B.; Ihle, J.N.
 Mol. Cell. Biol. 11, 2391-2398, 1991
 A:Title: Hematopoietic cells express two forms of lyn kinase differing by 21 amino acids
 A:Reference number: A39750; WUID:91203857; PMID:2017160
 A:Accession: A39750
 A:Molecule type: mRNA
 A:Residues: 1-24,46-76,'F',78-160,'I',162-278,'I',280-390,'I',392-424,'D',426-512 <YI1>
 A:Cross-references: GB:M57696; NID:9198940; PIDD:AAA39471.1; PID:9198941
 A:Molecule type: mRNA
 A:Residues: 1-24,46-76,'F',78-160,'I',162-278,'I',280-390,'I',392-424,'D',426-512 <YI2>
 A:Cross-references: GB:M57697; NID:9198942; PIDD:AAA39472.1; PID:9198943
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology, SH2 homology, SH3 homology
 C:Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprotease
 F:1-512/Product: protein-tyrosine kinase lym, long splice form #status predicted <WAT>
 F:1-24,46-512/Product: protein-tyrosine kinase lym, short splice form #status predicted
 F:70-118/Domain: SH3 homology <SH3>
 F:129-226/Domain: SH2 homology <SH2>
 F:245-504/Domain: protein kinase homology <KIN>
 F:253-261/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:2/5/Active site: lys #status predicted
 F:397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 3.1%; Score 8; DB 1; Length 512;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 116 GAFILRES 123
 Db 151 GAFILRES 158

Oy 116 GAFILRES 123
 Db 151 GAFILRES 158

RESULT 16

A:Molecule type: mRNA
 A:Residues: 1-512 <RES>
 A:Cross-references: GB:U16132; NID:9556287; PIDD:AAA65197.1; PID:9777773
 R:Thyerson, M.; Albrecht, D.; Zurcher, G.; Andres, A.C.; Ziemiecki, A.
 Biochem. Biophys. Res. Commun. 209, 582-589, 1995
 A:Title: Iyk, a novel intracellular protein tyrosine kinase differentially expressed in
 A:Reference number: 148608; MUID:9521656; PMID:7733928
 A:Accession: 148608
 A:Molecule type: mRNA
 A:Residues: 1-153,'I',155-236,'H',238-512 <RES2>
 A:Cross-references: EMBL:Z48757; NID:9736263; PIDD:CAA8658.1; PID:9736264
 C:Genetic: BSK
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology, SH2 homology, SH3 homology
 C:Keywords: ATP; blocked amino end; intestine; lipoprotein; myristylation; phosphotransferase
 F:56-112/Domain: SH3 homology <SH3>
 F:123-215/Domain: SH2 homology <SH2>
 F:239-501/Domain: protein kinase homology <KIN>
 F:247-255/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:5/Binding site: palmitate (Cys) (covalent) #status predicted
 F:269/Active site: lys #status predicted

Query Match 3.1%; Score 8; DB 2; Length 512;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 116 GAFILRES 123
 Db 145 GAFILRES 152

RESULT 17

A43807
 A:Molecule type: mRNA
 A:Residues: 1-517 <KIN>
 A:Cross-references: GB:X52191; NID:950395; PIDD:CAA36437.1; PID:950396
 A:Experimental source: monocytic tumor cell line from strain Balb/c
 R:Yi, T.L.; Williams, C.L.
 Oncogene 4, 1081-1087, 1989
 A:Title: Cloning of the murine c-fgr proto-oncogene cDNA and induction of c-fgr expression
 A:Reference number: S10072; MUID:89385605; PMID:2674853
 A:Accession: S10072
 A>Status: preliminary

A.Molecule type: mRNA
 A.Residues: 1-40, 'N', 42-211, 'Q', 213-517 <YTA>
 A.Cross-references: EMBL:X16440; NID:G50393; PIDD:CAA34463.1; PID:G50394
 C.Superfamily: protein-tyrosine kinase src; protein kinase homology; SH3 h
 C.Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phc
 F.132-229/Domain: SH3 homology <SH3>
 F.249-507/Domain: protein kinase homology <KIXX>
 F.257-265/Region: protein kinase ATP-binding motif
 F.279/Active site: myristylated amino end (Gly) (in mature form) #status predicted
 F.511/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 3.1%; Score 8; DB 2; Length 517;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFLIRS 123
 DB 154 GAFLIRS 161

RESULT 18
 S24547
 protein-tyrosine kinase (EC 2.7.1.112) fgr - rat
 C.Species: Rattus norvegicus (Norway rat)
 C.Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 18-Feb-2000
 C.Accession: S24547; PT0200
 R.Yue, C.C.
 submitted to the EMBL Data Library, December 1990
 A.Reference number: S24547
 A.Accession: S24547
 A.Status: preliminary
 A.Molecule type: mRNA
 A.Residues: 1-517 <YTB>
 A.Cross-references: EMBL:X57018; NID:G56145; PIDD:CAA40337.1; PID:G56146
 R.Yue, C.C.
 Mol. Immunol. 28, 399-408, 1991
 A.Title: Novel putative protein kinase clones from a rat large granular lymphocyte tumor
 A.Reference number: PT0196; MUID:91287726; PMID:2062320
 A.Accession: PT0200
 A.Molecule type: mRNA
 A.Residues: 371-427 <YU2>
 A.Experimental source: lymphocyte cell line
 C.Genetics:
 A.Gene: FGR
 C.Superfamily: protein-tyrosine kinase src; protein kinase homology; SH3 h
 C.Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phc
 F.132-229/Domain: SH3 homology <SH3>
 F.249-507/Domain: protein kinase homology <KIN>
 F.257-265/Region: protein kinase ATP-binding motif
 F.279/Active site: myristylated amino end (Gly) (in mature form) #status predicted
 F.511/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 3.1%; Score 8; DB 2; Length 517;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFLIRS 123
 DB 154 GAFLIRS 161

RESULT 19
 TYHUR
 protein-tyrosine kinase (EC 2.7.1.112) fgr - human
 N.Alternate names: kinase-related transforming protein (fgr)
 C.Species: Homo sapiens (man)
 C.Date: 31-Dec-1988 #sequence_revision 30-Sep-1989 #text_change 21-Jul-2000
 C.Accession: A27676; A28353; A24842; A45930; S24306
 R.Katamine, S.; Notario, V.; Rao, C.D.; Mikl, T.; Cheah, M.S.C.; Tronick, S.R.; Robbins,

Mol. Cell. Biol. 8, 259-266, 1988
 A.Title: Primary structure of the human fgr proto-oncogene product p55(c-fgr).
 A.Reference number: A27676; MUID:8094395; PMID:3275868
 A.Accession: A27676
 A.Molecule type: mRNA
 A.Residues: 1-529 <REA>
 A.Cross-references: GB:M19722; GB:J03429; NID:G182573; PIDD:AAA52451.1; PID:G182574
 R.Iinone, K.; Ikawa, S.; Samba, K.; Sukegawa, J.; Yamamoto, T.; Toyoshima, K.
 Oncogene 1, 301-304, 1987
 A.Title: Isolation and sequencing of cDNA clones homologous to the v-fgr oncogene from e
 A.Reference number: A28353; MUID:88262220; PMID:3330776
 A.Accession: A28353
 A.Molecule type: mRNA
 A.Residues: 1-143 <INO>
 R.Nishizawa, M.; Samba, K.; Yoshida, M.C.; Yamamoto, T.; Sasaki, M.; Toyoshima, K.
 Mol. Cell. Biol. 6, 511-517, 1986
 A.Title: Structure, expression, and chromosomal location of the human c-fgr gene.
 A.Reference number: A24842; MUID:87064334; PMID:3023853
 A.Accession: A24842
 A.Molecule type: DNA
 A.Residues: 111-416 <REB>
 A.Cross-references: GB:M12724; NID:G182581; PIDD:AAA52762.1; PID:G553286
 R.Brickell, P.M.; Patel, M.
 Br. J. Cancer 58, 704-709, 1988
 A.Title: Structure and expression of c-fgr proto-oncogene mRNA in Epstein-Barr virus conv
 A.Reference number: A45930; MUID:89134667; PMID:2852026
 A.Accession: A45930
 A.Molecule type: mRNA
 A.Residues: 1-177/524-529 <BRI>
 A.Cross-references: GB:M27454
 R.Patel, M.; Leavers, S.J.; Brickell, P.M.
 Oncogene 5, 201-206, 1990
 A.Title: Structure of the complete human c-fgr proto-oncogene and identification of mult
 A.Reference number: S24306; MUID:90206622; PMID:1690869
 A.Accession: S24306
 A.Status: translation not shown
 A.Molecule type: DNA
 A.Residues: 1-142 <PAT>
 A.Cross-references: EMBL:X52207; NID:G29893; PIDD:CAA36457.2; PID:G6006522
 C.Genetics:
 A.Gene: GDB:FCR
 A.Cross-references: GDB:120615; OMIM:164940
 A.Map position: 1p36.2-1p36.1
 C.Function:
 A.Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
 C.Superfamily: protein-tyrosine kinase src; protein kinase homology; SH3 h
 C.Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phc
 in kinase
 F.84-133/Domain: SH3 homology <SH3>
 F.144-241/Domain: SH2 homology <SH2>
 F.261-519/Domain: protein kinase homology <KIN>
 F.269-277/Region: protein kinase ATP-binding motif
 F.2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F.3.6/Binding site: palmitate (Cys) (covalent) #status predicted
 F.291/Active site: lys #status predicted
 F.523/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 3.1%; Score 8; DB 1; Length 529;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFLIRS 123
 DB 166 GAFLIRS 173

RESULT 20
 A44991
 protein-tyrosine kinase (EC 2.7.1.112) fyn (similarity) - mouse
 N.Alternate names: kinase-related transforming protein (fyn)
 C.Species: Mus musculus (house mouse)
 C.Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 16-Jun-2000
 C.Accession: A44991

R:Cooke, M.P.; Perlmutter, R.M.

New Biol. 1, 66-74, 1989

A:Title: Expression of a novel form of the fyn proto-oncogene in hematopoietic cells.

A:Reference number: A44991; MUID:91175680; PMID:2488273

A:Accession: A44991

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-534 <COO>

A:Cross-references: GB:M27266; NID:g193357; PIDN:AAA37644.1; PID:g309241

A>Note: in the authors' translation an additional residue Leu was shown after Lys, for

C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phd

F:89-138/Domain: SH3 homology <SH3>

F:149-246/Domain: SH2 homology <SH2>

F:266-524/Domain: protein kinase homology <KIN>

F:274-282/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:296/Active site: Lys #status predicted

F:417.528/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match

Best Local Similarity 3.1%; Score 8; DB 1; Length 534;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 118 FLIRESOT 125

DB 173 FLIRESOT 180

RESULT 21

T30021

hypothetical protein K08F11.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T30021

R:Murray, J.; Wohlmann, P.

submitted to the EMBL Data Library, September 1996

A:Description: The sequence of C. elegans cosmid K08F11.

A:Reference number: Z20723

A:Accession: T30021

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-575 <MUR>

A:Cross-references: EMBL:U070855; PIDN:AA09162.1; GSPDB:GN00022; CESP:K08F11.4

A:Experimental source: strain Bristol N2; clone K08F11

C:Genetics:

A:Gene: CESP:K08F11.4

A:Map position: 4

A:Introns: 19/2; 53/2; 111/1; 156/3; 379/3; 440/1

Query Match

Best Local Similarity 3.1%; Score 8; DB 2; Length 575;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 103 KAEELL 110

DB 289 KAEELL 296

RESULT 22

T38674

probable membrane transport protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T38674

R:Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, May 1997

A:Reference number: Z21772

A:Accession: T38674

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-743 <BAD>

A:Cross-references: EMBL:Z95395; PIDN:CA080751.1; GSPDB:GN00066; SPDB:SPAC3A12.06C

A:Experimental source: strain 972h-; cosmid c3A12

C:Genetics:

A:Gene: SPDB:SPAC3A12.06C

A/Map position: 1

Query Match

Best Local Similarity 3.1%; Score 8; DB 2; Length 743;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 LPSPSLSS 18

DB 455 LPSPSLSS 462

RESULT 23

D48059

oncoprotein zN-MYC - zebra fish (fragment)

C:Species: Brachydanio rerio (zebra fish)

C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-May-1997

C:Accession: D48059

R:Schreiber-Agus, N.; Horner, J.; Torres, R.; Chiu, F.C.; Depinho, R.A.

Mol. Cell. Biol. 13, 2765-2775, 1993

A:Title: Zebra fish myc family and max genes: differential expression and oncogenic acti

A:Reference number: A48059; MUID:93233639; PMID:8474440

A:Accession: D48059

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-93 <SCH>

A>Note: sequence extracted from NCBI backbone (NC81P:129811)

C:Superfamily: MYC transforming protein; MYC transforming protein homology

F:1-93/Domain: MYC transforming protein homology (fragment) <MYC>

Query Match

Best Local Similarity 2.7%; Score 7; DB 2; Length 93;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 106 ELLLP 112

DB 52 ELLLP 58

RESULT 24

S77055

hypothetical protein s110669 - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

A:Variety: PCC 6803

C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C:Accession: S77055

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 103-126, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

S.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S77055

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-106 <KAN>

A:Cross-references: EMBL:D64005; GB:AB001339; NID:g1001779; PIDN:BA10747.1; PID:d101135

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match

Best Local Similarity 2.7%; Score 7; DB 2; Length 106;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 SPSPSS 19

DB 85 SPSPSS 91

RESULT 25

T44547

hypothetical protein PA0624 (imported) - Pseudomonas aeruginosa

C/Species: *Pseudomonas aeruginosa*
 C/Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 31-Dec-2000
 C/Accession: T44547; F83567
 R/Octenweil, B.; Ishihara, H.; Shiomura, T.; Kageyama, M.; Kanaya, S.; Oh
 submitted to the EMBL Data Library, August 1999
 A/Description: Genetic relationship between bacteriocins and bacteriophages.
 A/Reference number: Z22790
 A/Accession: T44547
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-114 <NAK>
 A/Cross-references: EMBL:AB030825; PIDN:BAAB3162.1
 A/Experimental source: strain PA01
 R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Larbig, K.; Lim,
 .; Loty, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
 A/Reference number: AB2950; WUID:20437337; PMID:10984043
 A/Accession: F83567
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-114 <STO>
 A/Cross-references: GB:AE004498; GB:AE004091; NID:99946491; PIDN:AA004013.1; GSPDB:GN001
 A/Experimental source: strain PA01
 C/Genetics:
 A/Gene: PA0624

Query Match 2.7%; Score 7; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 134 VRLSRPA 140
 DB 20 VRLSRPA 26

RESULT 26
 AB1172
 hypothetical protein lmo0778 [imported] - *Listeria monocytogenes* (strain EGD-e)
 C/Species: *Listeria monocytogenes*
 C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C/Accession: AB1172
 R/Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
 .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Feih, H.
 D.; Jones, L.M.; Karet, U.
 Science 294, 849-852, 2001
 A/Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schlueter, T.; Simoes, N.; Tietzer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend
 A/Title: Comparative genomics of *Listeria* species
 A/Reference number: AB1077; WUID:21537279; PMID:11679669
 A/Accession: AB1172
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-115 <GLA>
 A/Cross-references: GB:NC_003210; PIDN:CAC98856.1; PID:G16410167; GSPDB:GN00177
 A/Experimental source: strain EGD-e
 C/Genetics:
 A/Gene: lmo0778

Query Match 2.7%; Score 7; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 144 RIRHYRI 150
 DB 64 RIRHYRI 70

RESULT 27
 T17315
 hypothetical protein DKFZp434K058.1 - human
 C/Species: *Homo sapiens* (man)

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C/Accession: T17315
 R/Octenweil, B.; Obermaier, B.; Mewes, H.W.; Gaesshuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, September 1999
 A/Reference number: Z18726
 A/Accession: T17315
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-117 <OTT>
 A/Cross-references: EMBL:AL117583
 A/Experimental source: adult testis, clone DKFZp434K058
 C/Genetics:
 A/Note: DKFZp434K058.1

Query Match 2.7%; Score 7; DB 2; Length 117;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 164 LTFPSLQ 170
 DB 34 LTFPSLQ 40

RESULT 28
 AC1449
 hypothetical protein lln0130 [imported] - *Listeria innocua* (strain Clp11262)
 C/Species: *Listeria innocua*
 C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C/Accession: AC1449
 R/Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
 .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Feih, H.
 D.; Jones, L.M.; Karet, U.
 Science 294, 849-852, 2001
 A/Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maitournam, A.; M
 ok, C.; Schlueter, T.; Simoes, N.; Tietzer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend
 A/Title: Comparative genomics of *Listeria* species
 A/Reference number: AB1077; WUID:21537279; PMID:11679669
 A/Accession: AC1449
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-118 <GLA>
 A/Cross-references: GB:AL592022; PIDN:CAC95363.1; PID:G16412549; GSPDB:GN00178
 A/Experimental source: strain Clp11262
 C/Genetics:
 A/Gene: lln0130

Query Match 2.7%; Score 7; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 144 RIRHYRI 150
 DB 65 RIRHYRI 71

RESULT 29
 A48837
 subgroup A Rous sarcoma virus receptor, splice form 1 - Japanese quail
 N/Alternate names: low density lipoprotein receptor-related protein
 C/Species: *Coturnix coturnix japonica* (Japanese quail)
 C/Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997
 C/Accession: A48837
 R/Bates, P.; Young, J.A.; Varnus, H.E.
 Cell 74, 1043-1051, 1993
 A/Title: A receptor for subgroup A Rous sarcoma virus is related to the low density lip
 A/Reference number: A48837; WUID:94006516; PMID:8402880
 A/Accession: A48837
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-120 <BAT>
 A/Experimental source: QT6 cells
 A/Note: sequence extracted from NCBI backbone (NCBIN:138481, NCBI:138483)
 C/Superfamily: LDL receptor ligand-binding repeat homology

F:30-69/Domain: LDL receptor ligand-binding repeat homology <LDL2>

Query Match

Best Local Similarity 2.7%; Score 7; DB 2; Length 120;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 LLLLPGN 113
DB 10 LLLLPGN 16

RESULT 30

H82763
hypothetical protein XE0770 [imported] - *Xylella fastidiosa* (strain 9a5c)

C/Species: *Xylella fastidiosa*
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C/Accession: H82763

R:Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing

A/Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A/Reference number: A82515; PMID:20365717; PMID:10910347

A/Note: for a complete list of authors see reference number A59328 below

A/Accession: H82763
A/Status: preliminary
A/Molecule type: DNA

A/Residues: 1-136 <SIM>
A/Cross-references: GB:AE003918; GB:AE003849; NID:G9105662; PIDN:AAF83580.1; GSPDB:GN001

A/Experimental source: strain 9a5c
R:Stimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briano, M.R.S.; Bueno, M.R.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, H
as-Neco, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000

A/Author: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; From
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krüger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martins, C.L.; Marques, M.V.; Martins, E
A/Author: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Mitracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.N
Rodrigues, V.; Rosa, A.J. de M.; de Rosa, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Trunsko, M.H.; Vallada, H.; Van Sluys, W.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A/Reference number: A59328
A/Contents: annotation
A/Genetics:

A/Map position: circular chromosome
A/Map position: circular chromosome

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A/Map position: circular chromosome
A/Map position: circular chromosome

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 PPSPLS 18
DB 97 PPSPLS 103

RESULT 32

PC4110
transcription regulator homolog - *Streptomyces aureofaciens* (fragment)

N/Alternate names: hypothetical 137 protein
C/Species: *Streptomyces aureofaciens*

C/Date: 10-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 06-Oct-2000
C/Accession: PC4110

R:Kormanec, J.; Lempelova, A.; Farkasovsky, M.; Homerova, D.
Gene 165, 77-80, 1995

A/Title: Cloning, sequencing and expression in *Escherichia coli* of a *Streptomyces aureofaciens*

A/Reference number: J43733; PMID:96084956; PMID:7489920

A/Accession: PC4110
A/Molecule type: DNA

A/Residues: 1-137 <KOR>
A/Cross-references: GB:U21191; NID:G706951; PIDN:AAA91363.1; PID:G706952

A/Comment: This protein has a helix-turn-helix DNA-binding domain in the carboxyl-termin
C/Suprafamily: Mycobacterium tuberculosis hypothetical protein Rv1931c
C/Keywords: transcription

Query Match
Best Local Similarity 2.7%; Score 7; DB 2; Length 137;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 RLGPPLT 60
DB 43 RLGPPLT 49

RESULT 33

E97462
organic hydroperoxide resistance protein (PA2850) [imported] - *Agrobacterium tumefaciens*

C/Species: *Agrobacterium tumefaciens*
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C/Accession: E97462

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ouroulo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001

A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*

A/Reference number: A73539; PMID:11743194

A/Accession: E97462
A/Status: preliminary
A/Molecule type: DNA

A/Residues: 1-140 <KOR>
A/Cross-references: GB:AE007869; PIDN:AAK86654.1; PID:G15155834; GSPDB:GN00169

A/Genetics:
A/Map position: circular chromosome

A/Map position: circular chromosome
A/Map position: circular chromosome

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A/Map position: circular chromosome
A/Map position: circular chromosome

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: Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AG2680
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140 <KUR>
A:Cross-references: GB:AE006688; PIDN:ALA41861.1; PID:gl7739222; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu0847
A:Map position: circular chromosome
C:Superfamily: hypothetical protein yk1A

Query Match          2.7% Score 7; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 REKAEL 107
    |||||
Db 109 REKAEL 115

RESULT 35
subgroup A Rous sarcoma virus receptor, splice form 2 - Japanese quail
M:Alternate names: low density lipoprotein receptor-related protein
C:Species: Coturnix coturnix japonica (Japanese quail)
C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997
C:Accession: B48837
R:Bates, P.; Young, J.A.; Varmus, H.E.
Cell 74, 1043-1051, 1993
A>Title: A receptor for subgroup A Rous sarcoma virus is related to the low density lipop
A:Reference number: A48837; MUID:94006516; PMID:8402880
A:Accession: B48837
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-157 <BAT>
A:Experimental source: OR6 cells
A>Note: sequence inconsistent with nucleotide translation
C:Superfamily: LDL receptor ligand-binding repeat homology
F:30-69/Domain: LDL receptor ligand-binding repeat homology <LDL2>

Query Match          2.7% Score 7; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 LLLLPN 113
    |||||
Db 10 LLLLPN 16

RESULT 36
T9489
related to H+-transporting ATP synthase protein 6 [imported] - Neurospora crassa
M:Alternate names: protein B1406.410
C:Species: Neurospora crassa
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T9489
R:Schulte, U.; Aign, V.; Hohenfeld, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nykataru,
submitted to the Protein Sequence Database, May 2000
A:Reference number: 225022
A:Accession: T9489
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-166 <SCH>
A:Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B1406.410
A:Experimental source: BAC clone B1406; strain OR74A
C:Genetics:

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A:Gene: NCSP:B1406.410
A:Map position: 6

```

```

Query Match          2.7% Score 7; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 127 RGSYSLS 133
    |||||
Db 15 RGSYSLS 21

```

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RESULT 37
C83573

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hypothetical protein PA0583 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83573

```

```

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapid, K.; Lim
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: C83573

```

```

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-180 <STO>
A:Cross-references: GB:AE004494; GB:AE004091; NID:99946446; PIDN:AA03972.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0583

```

```

Query Match          2.7% Score 7; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 49 AELSLRL 55
    |||||
Db 66 AELSLRL 72

```

```

RESULT 38
F95944

```

```

hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplaemid pSymB
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: F95944

```

```

R:Finan, T.M.; Weiner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar
proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A>Title: The complete sequence of the 1,683-kb pSymB magaplaemid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: F95944

```

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A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-188 <KUR>

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```

A:Cross-references: GB:AL591985; PIDN:CA049222.1; PID:915140708; GSPDB:GN00167
A:Experimental source: strain 1021, magaplaemid pSymB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Punler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pla, D.; Chain, P.; Cowie, A.; Davls, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
beault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A>Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104

```

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A:Contents: annotation
C:Genetics:
A:Gene: Smb21156
A:Genome: plasmid

```

```

Query Match          2.7% Score 7; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 54;

```

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 RUTFPST 169
|||||
DB 88 RUTFPST 94

RESULT 39

T46076

hypothetical protein T20E23.50 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 20-Jun-2000

C/Accession: T46076

R/Author: M.; Perez-Perez, A.; Terol, J.; Torres, A.; Perez-Alonso, M.; Mewes, H.W.; Le

submitted to the Protein Sequence Database, December 1999

A/Reference number: 223020

A/Accession: T46076

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-189 <BAR>

A/Cross-references: EMBL:AL133363

A/Experimental source: cultivar Columbia, BAC clone T20E23

C/Genetics:

A/Map position: 3

A/Intons: 99/2

A/Note: T20E23.50

C/Superfamily: Arabidopsis thaliana hypothetical protein T20E23.60

Query Match 2.7%; Score 7; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 KETDSSL 224
|||||
DB 105 KETDSSL 111

RESULT 40

C75194

hypothetical protein PAB2291 - Pyrococcus abyssi (strain Orsay)

C/Species: Pyrococcus abyssi

C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C/Accession: C75194

R/Anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru

A/Reference number: A75001

A/Accession: C75194

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-193 <KAM>

A/Cross-references: GB:AJ248283; GB:AL096836; NID:G5457433; PIDN:CAM49002.1; PID:G545751

A/Experimental source: strain Orsay

C/Genetics:

A/Map position: I

A/Intons: 99/2

A/Note: T20E23.50

C/Superfamily: conserved hypothetical protein M01150

Query Match 2.7%; Score 7; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 SREKAE 106
|||||
DB 154 SREKAE 160

RESULT 41

T37263

probable tyrosine kinase receptor R09D1.12 - Caenorhabditis elegans (fragment)

C/Species: Caenorhabditis elegans

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 26-May-2000

C/Accession: T37263

R/Author: G.; Roubin, R.; Coulier, F.; Pontarotti, P.; Birnbaum, D.

submitted to the EMBL Data Library, September 1999

A/Reference number: 221654

A/Accession: T37263

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-198 <POP>

A/Cross-references: EMBL:AF186748; PIDN:AAF00545.1

A/Experimental source: strain N2

C/Genetics:

A/Map position: I

A/Intons: 99/2

A/Note: T20E23.50

C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match 2.7%; Score 7; DB 2; Length 198;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 VSGREYN 81
|||||
DB 183 VSGREYN 189

RESULT 42

F71495

probable n-acetylmuramoyl-L-Ala amidase - Chlamydia trachomatis (serotype D, strain UW3/

C/Species: Chlamydia trachomatis

C/Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 18-Aug-2000

C/Accession: F71495

R/Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,

Science 282, 754-759, 1998

A/Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac

A/Reference number: A71570; MUID:99000809; PMID:9784136

A/Accession: F71495

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-200 <ARN>

A/Cross-references: GB:AE001330; GB:AE001273; NID:G3329034; PIDN:AA068203.1; PID:G332904

A/Experimental source: serotype D, strain UW-3/CX

C/Genetics:

A/Map position: I

A/Intons: 99/2

A/Note: T20E23.50

C/Superfamily: conserved hypothetical protein TC0890

Query Match 2.7%; Score 7; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 STQALVD 174
|||||
DB 129 STQALVD 135

RESULT 43

H81653

conserved hypothetical protein TC0890 [imported] - Chlamydia muridarum (strain Nigg)

C/Species: Chlamydia muridarum, Chlamydia trachomatis Mopn

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 18-Aug-2000

C/Accession: H81653

R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,

C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A/Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.

A/Reference number: A81500; MUID:20150255; PMID:10684935

A/Accession: H81653

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-202 <TET>

A/Cross-references: GB:AE002355; GB:AE002160; NID:G7190911; PIDN:AA93665.1; PID:G719093

A/Experimental source: strain Nigg (Mopn)

C/Genetics:

A/Map position: I

A/Intons: 99/2

A/Note: T20E23.50

C/Superfamily: conserved hypothetical protein TC0890

Query Match 2.7%; Score 7; DB 2; Length 202;

Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 SLQALVD 174
|||||
Db 131 SLQALVD 137

RESULT 44

B60030

gene B protein - alcelaphine herpesvirus 1 (strain WC11) (fragment)

C.Species: alcelaphine herpesvirus 1

C.Date: 28-Apr-1993 #sequence_revision 30-Sep-1993 #text_change 26-May-2000

C.Accession: B60030

R.Hsu, D.; Shih, L.M.; Zee, Y.C.

Arch. Virol. 113, 53-60, 1990

A.Title: Nucleotide sequence of a 3.5 kilobase fragment of malignant catarrhal fever vir

A.Reference number: A60030; MUID:90351277; PMID:2167059

A.Accession: B60030

A.Molecule type: DNA

A.Residues: 1-210 <STO>

C.Superfamily: herpesvirus glycoprotein H

Query Match 2.7%; Score 7; DB 2; Length 210;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 AEEHLL 110
|||||
Db 85 AEEHLL 91

RESULT 45

B85816

unknown protein encoded within prophage CP-933U (imported) - Escherichia coli (strain O1

C.Species: Escherichia coli

C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C.Accession: B85816

R.Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaeser, J.D.; Rose, D.J.; Mayhew

iller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A.Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A.Reference number: A85480; MUID:21074935; PMID:11206551

A.Accession: B85816

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-217 <STO>

A.Cross-references: GB:AE005174; NID:g12516088; PIDN:AGS6990.1; GSPDB:GN00145; UWGP:230

C.Experimental source: strain O157:H7, substrain EDL933

C.Genetics:

A.Gene: Z3071

Query Match 2.7%; Score 7; DB 2; Length 217;

Best Local Similarity 100.0%; Pred. No. 62;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 SLRGGP 58
|||||
Db 191 SLRGGP 197

RESULT 46

B90968

hypothetical protein Ec82714 [imported] - Escherichia coli (strain O157:H7, substrain R1

C.Species: Escherichia coli

C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

C.Accession: B90968

R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gawaray, N.; Yasunaga, T.; Kohara, S.; Shiba, T.; Hattori, M.; Shimagawa, H.

DNA Res. 8, 11-22, 2001

A.Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno

A>Status: preliminary

A.Molecule type: DNA

A.Residues: 1-217 <HAV>

A.Cross-references: GB:BA000007; PIDN:BA836137.1; PID:g13362182; GSPDB:GN00154

A.Experimental source: strain O157:H7, substrain R1MD 0509952

C.Genetics:

A.Gene: Ec82714

Query Match 2.7%; Score 7; DB 2; Length 217;

Best Local Similarity 100.0%; Pred. No. 62;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 SLRGGP 58
|||||
Db 191 SLRGGP 197

RESULT 47

A86649

hypothetical protein yjbJ [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C.Species: Lactococcus lactis subsp. lactis

C.Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C.Accession: A86649

R.Bolotin, A.; Winkler, P.; Manger, S.; Jallou, O.; Malarme, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A.Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s

A.Reference number: A86625; MUID:21235186; PMID:11337471

A.Accession: A86649

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-219 <STO>

A.Cross-references: GB:AE005176; PID:g12723047; PIDN:AKK04291.1; GSPDB:GN00146

C.Experimental source: strain IL1403

C.Genetics:

A.Gene: yjbJ

Query Match 2.7%; Score 7; DB 2; Length 219;

Best Local Similarity 100.0%; Pred. No. 62;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 220 LBSLLF 226
|||||
Db 89 LBSLLF 95

RESULT 48

A12759

arsenical resistance protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C.Species: Agrobacterium tumefaciens

C.Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002

C.Accession: A12759

R.Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuyavlin, T.; Levy, R.; Li, M.; McClell

; Kap, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A.Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krepan, W.; Perry, M.; Gordon-Kamm,

er, B.W.

A.Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A.Reference number: AB2577; PMID:11743193

A.Accession: A12759

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-236 <KOR>

A.Cross-references: GB:AE008688; PIDN:AL42495.1; PID:g17739913; GSPDB:GN00186

A.Experimental source: strain C58 (Dupont)

C.Genetics:

A.Gene: arsH

A.Map position: circular chromosome

Query Match 2.7%; Score 7; DB 2; Length 236;

Best Local Similarity 100.0%; Pred. No. 67;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 165 TFPSLQA 171
 |||||
 Db 4 TFPSLQA 10

RESULT 49

G75422
 hypothetical protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: G75422
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: G75422
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-245 <WHI>
 A:Cross-References: GB:AE001970; GB:AE000513; NID:96458956; PIDN:AAFI0799.1; PID:9645897
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR1221
 A:Map position: 1

Query Match

Best Local Similarity 2.7%; Score 7; DB 2; Length 245;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 RLGEPLT 60
 |||||
 Db 22 RLGEPLT 28

RESULT 50

G97540
 arabin-like protein (AF173880) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
 C:Species: Agrobacterium tumefaciens
 C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
 C:Accession: G97540
 R:Godner, B.; Hinkle, G.; Gatlung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: A97359; PMID:11743194
 A:Accession: G97540
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-248 <KUR>
 A:Cross-References: GB:AE007869; PIDN:AAK87280.1; PID:G15156572; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR_C_2746
 A:Map position: circular chromosome

Query Match

Best Local Similarity 2.7%; Score 7; DB 2; Length 248;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 165 TFPSLQA 171
 |||||
 Db 16 TFPSLQA 22

Search completed: March 24, 2003, 16:08:36
 Job time : 30 secs